

Application No.: 10/028,482

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

Claim 1 (currently amended). A system for high throughput detection of genotypes comprising:

a sample preparation method comprising a method for amplifying a plurality of regions of interest using a method comprising long range polymerase chain reaction amplification of a plurality of nucleic acid samples to form a plurality of amplicons wherein the amplicons are 3 to 15 kilobases and a method for pooling aliquots of a plurality of the amplicons into a plurality of pooled samples for hybridization;

a sample preparation automation system;

a sample tracking system;

an automated high density probe array loader comprising a robotic arm and a refrigerated unit;

a plurality of high density nucleic acid probe arrays wherein each array comprises about 400,000 different sequence probes, wherein each probe is present in a different feature of the array;

a computer system for managing hybridization data and for analyzing hybridization data to determine the genotype of a sample at a plurality of single nucleotide polymorphisms in a region of interest, wherein said hybridization data are is obtained by hybridizing a pooled sample to a high density nucleic acid probe array.

Claim 2 (previously presented). The system of claim 1 wherein the sample preparation automation system is a robotic device for handling multiwell plates.

Claim 3 (original). The system of claim 1 wherein the sample tracking system is a bar code system.

Application No.: 10/028,482

Claim 4 (previously presented). The system of Claim 1 wherein the computer system comprises a processor; and a memory being coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform the step of analyzing the hybridization data to determine the genotype of a sample at a plurality of single nucleotide positions in a region of interest.

Claims 5-16 (canceled).

Claim 17 (previously presented). The system of claim 1 wherein the sample tracking system and the computer system are linked.

Claim 18 (canceled)

Claim 19 (canceled)

Claim 20 (currently amended). The system of claim ~~18~~ 1 wherein prior to long range polymerase chain reaction amplification each nucleic acid sample is reverse transcribed to obtain cDNA.

Claim 21 (previously presented). The system of claim 1 wherein said probe arrays have feature sizes of about 20 x 24 microns or smaller.

Claim 22 (currently amended). The system of claim 21 wherein each high density nucleic acid probe array is capable of simultaneous screening of about 30 kilobases of sense nucleic acid sequence and about 30 kilobases of antisense nucleic acid sequence.

Claim 23 (previously presented). The system of claim 1 wherein the high density nucleic acid probe arrays are resequencing or variation detection arrays.

Claim 24 (previously presented). The system of claim 1 wherein the high density nucleic acid probe arrays genotype a plurality of single nucleotide polymorphisms.

Application No.: 10/028,482

Claim 25 (previously presented). The system of claim 1 wherein a contiguous sequence is tiled on the high density nucleic acid probe arrays.

Claim 26 (previously presented). The system of claim 1 wherein the sample tracking system comprises a single or multiple dimensional barcode system.

Claim 27 (previously presented). The system of claim 1 wherein the sample tracking system comprises an electromagnetic encoding system.